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 NEWS  4  Feb 16  TOXLINE no longer being updated
 NEWS  5  Apr 23  Search Derwent WPINDEX by chemical structure
 NEWS  6  Apr 23  PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
 NEWS  7  May 07  DGENE Reload
 NEWS  8  Jun 20  Published patent applications (A1) are now in USPATFULL

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FILE 'HOME' ENTERED AT 13:14:58 ON 21 JUN 2001

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FILE 'MEDLINE' ENTERED AT 13:15:31 ON 21 JUN 2001

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FILE 'BIOSIS' ENTERED AT 13:15:31 ON 21 JUN 2001
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=> s oxazolidinone

L1 8295 OXAZOLIDINONE

=> s elongation factor p

L2 104 ELONGATION FACTOR P

=> s efp

L3 755 EFP

=> s l2 and l3

L4 16 L2 AND L3

=> d l4 ti abs ibib tot

L4 ANSWER 1 OF 16 MEDLINE
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and
Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to **elongation factor P**, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and

replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that **elongation factor P** is important but not essential for the growth of Agrobacterium.

ACCESSION NUMBER: 2001086878 MEDLINE
DOCUMENT NUMBER: 20566665 PubMed ID: 11114898
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR: Peng W T; Banta L M; Charles T C; Nester E W
CORPORATE SOURCE: Department of Microbiology, University of Washington, Seattle, Washington 98195-7242, USA.
CONTRACT NUMBER: GM32618 (NIGMS)
SOURCE: JOURNAL OF BACTERIOLOGY, (2001 Jan) 183 (1) 36-45.
Journal code: HH3. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF177860
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered PubMed: 20001229
Entered Medline: 20010118

L4 ANSWER 2 OF 16 MEDLINE
TI The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis.
AB **Elongation factor P** (**EFP**) is a protein that stimulates the peptidyltransferase activity of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N-formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a homologous protein, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (KanR) gene was inserted near the N-terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temperature-sensitive origin of replication. After transformation into a recA+ E. coli strain, temperature-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants containing the **efp** -KanR gene in the chromosome grew at 33 degrees C only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44 degrees C. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44 degrees C. At 44 degrees C, mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for protein synthesis.

ACCESSION NUMBER: 1998070395 MEDLINE
DOCUMENT NUMBER: 98070395 PubMed ID: 9405429
TITLE: The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis.
AUTHOR: Aoki H; Dekany K; Adams S L; Ganoza M C
CORPORATE SOURCE: Banting and Best Department of Medical Research, Nucleic Acids, Protein Synthesis and Molecular Genetics, University of Toronto, Toronto, Ontario M5G 1L6, Canada.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Dec 19) 272 (51) 32254-9.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 19980130
Entered Medline: 19980122

L4 ANSWER 3 OF 16 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the activity of **efp** comprises contacting **efp** with a compound and determining whether the compound modifies activity of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the binding of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled oxazolidinone compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation

factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp** , the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an oxazolidinone compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN
COUNTRY COUNT: 86
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW

AU 9942246	A	20000818	(200057)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000045177	A1	WO 1999-US12073	19990528
AU 9942246	A	AU 1999-42246	19990528

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 200045177

PRIORITY APPLN. INFO: US 1999-117473 19990127

L4 ANSWER 4 OF 16 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and

Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through [redacted] sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to **elongation factor P**, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that **elongation factor P** is important but not essential for the growth of Agrobacterium.

ACCESSION NUMBER: 2001002700 EMBASE
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR: Peng W.-T.; Banta L.M.; Charles T.C.; Nester E.W.
CORPORATE SOURCE: E.W. Nester, Department of Microbiology, Box 357242, University of Washington, Seattle, WA 98195-7242, United States. gnester@u.washington.edu
SOURCE: Journal of Bacteriology, (2001) 183/1 (36-45).
Refs: 55
ISSN: 0021-9193 CODEN: JOBAAY
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 5 OF 16 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
TI The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis.
AB **Elongation factor P** (**EFP**) is a protein that stimulates the peptidyltransferase activity of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N- formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a homologous protein, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (Kan(R)) gene was inserted near the N- terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temperature-sensitive origin of replication. After transformation into a recA+ E. coli strain, temperature-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants containing the **efp** -Kan(R) gene in the chromosome grew at 33 .degree.C only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44 .degree.C. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44 .degree.C. At 44 .degree.C, mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for protein synthesis.

ACCESSION NUMBER: 1998006933 EMBASE
TITLE: The gene encoding the **elongation factor P** protein is essential for viability and is

required for protein synthesis.
AUTHOR: Aok[illegible].; Dekany K.; Adams S.-L.; Ganoza M.C.
CORPORATE SOURCE: M.C. Ganoza, C.H. Best Institute, Un[illegible]ersity of Toronto, Toronto, Ont. M5G 1L6, Canada. m.ganoza@utoronto.ca
SOURCE: Journal of Biological Chemistry, (1997) 272/51 (32254-32259).
Refs: 42
ISSN: 0021-9258 CODEN: JBCHA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 6 OF 16 DGENE COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
AB The present sequence is the Escherichia coli **elongation factor p** (**efp**), which comprises part of the prokaryotic ribosomal complex. It can be used in the methods of the invention to identify compounds which interfere with ribosomal peptide bond synthesis, which can then be used as antimicrobial agents. These compounds may modulate interactions between any of the ribosomal subunits, including the 30S and 50S subunits, as well as factors such as **efp** and L16. They can also be used to identify compounds which modulate the activity of **efp** but do not have any effect on its mammalian analogue eIF5A.
ACCESSION NUMBER: AAB21122 protein DGENE
TITLE: Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
INVENTOR: Poorman R A; Wells P A; Marotti K R; Shinabarger D L
PATENT ASSIGNEE: (PHAA) PHARMACIA & UPJOHN.
PATENT INFO: WO 2000045177 A1 20000803 52p
APPLICATION INFO: WO 1999-US12073 19990528
PRIORITY INFO: US 1999-117473 19990127
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2000-524303 [47]

L4 ANSWER 7 OF 16 DGENE COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
AB The present sequence is the Staphylococcus aureus **elongation factor p** (**efp**), which comprises part of the prokaryotic ribosomal complex. It can be used in the methods of the invention to identify compounds which interfere with ribosomal peptide bond synthesis, which can then be used as antimicrobial agents. These compounds may modulate interactions between any of the ribosomal subunits, including the 30S and 50S subunits, as well as factors such as **efp** and L16. They can also be used to identify compounds which modulate the activity of **efp** but do not have any effect on its mammalian analogue eIF5A.
ACCESSION NUMBER: AAB21121 protein DGENE
TITLE: Identifying a compound which modulates the activity of

prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
INVENTOR: Poorman R A; Wells P A; Marotti K R; Shinabarger D L
PATENT ASSIGNEE: (PHAA)PHARMACIA & UPJOHN.
PATENT INFO: WO 2000045177 A1 20000803 52p
APPLICATION INFO: WO 1999-US12073 19990528
PRIORITY INFO: US 1999-117473 19990127
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2000-524303 [47]

L4 ANSWER 8 OF 16 DGENE COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
AB The present sequence is an oligoribonucleotide used in an initiation complex assay to determine the effects of the presence and absence of the Staphylococcus aureus or Escherichia coli **elongation factor p** (**efp**). This protein comprises part of the prokaryotic ribosomal complex. It can be used in the methods of the invention to identify compounds which interfere with ribosomal peptide bond synthesis, which can then be used as antimicrobial agents. These compounds may modulate interactions between any of the ribosomal subunits, including the 30S and 50S subunits, as well as factors such as **efp** and L16. They can also be used to identify compounds which modulate the activity of **efp** but do not have any effect on its mammalian analogue eIF5A.
ACCESSION NUMBER: AAA76244 mRNA DGENE
TITLE: Identifying a compound which modulates the activity of prokaryotic **elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified -
INVENTOR: Poorman R A; Wells P A; Marotti K R; Shinabarger D L
PATENT ASSIGNEE: (PHAA)PHARMACIA & UPJOHN.
PATENT INFO: WO 2000045177 A1 20000803 52p
APPLICATION INFO: WO 1999-US12073 19990528
PRIORITY INFO: US 1999-117473 19990127
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2000-524303 [47]

L4 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2001 ACS
TI Crystallization and structure determination of Staphylococcus aureus **elongation factor P**
AB Staphylococcus aureus **elongation factor P** (S. aureus EF-P) was crystd., and the 3-dimensional x-ray crystal structure solved to 1.9 A resoln. EF-P crystals belong to the orthorhombic space group symmetry P212121, with dimensions of a = 25-50, b = 35-60, c = 85-110 .ANG. and .alpha. = .beta. = .gamma. = 90.degree.. The x-ray crystal structure is useful for solving the structure of other mols. or mol. complexes, and designing inhibitors of S. aureus EF-P.
ACCESSION NUMBER: 2001:115188 HCAPLUS
DOCUMENT NUMBER: 134:159195
TITLE: Crystallization and structure determination of Staphylococcus aureus **elongation**

factor P
INVENTOR(S): Benson, Timothy E.
PATENT ASSIGNEE(S): Pharmacia and Upjohn Company, U
SOURCE: PCT Int. Appl., 289 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001010906	A1	20010215	WO 2000-US21528	20000804

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-147851 P 19990806
REFERENCE COUNT: 9
REFERENCE(S):
(1) Aoki, H; BIOCHIMIE (PARIS) 1997, V79(1), P7 HCAPLUS
(2) Aoki, H; JOURNAL OF BIOLOGICAL CHEMISTRY 1997, V272(51), P32254 HCAPLUS
(4) Kim, K; PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES 1998, V95(18), P10419 HCAPLUS
(7) Marotti, K; WO 0045177 A 2000 HCAPLUS
(9) Zhou, Q; EMBO (EUROPEAN MOLECULAR BIOLOGY ORGANIZATION) JOURNAL 1998, V17(13), P3681 HCAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2001 ACS
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and
Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to **elongation factor P**, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The anal. of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern anal. suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that **elongation factor P** is important but not essential for the growth of Agrobacterium.
ACCESSION NUMBER: 2001:11527 HCAPLUS

TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis
AUTHOR(S): Peng, Wen-Tao; Banta, Lois M.; Charles, Trevor C.; Nester, Eugene W.
CORPORATE SOURCE: Department of Microbiology, University of Washington, Seattle, WA, 98195-7242, USA
SOURCE: J. Bacteriol. (2001), 183(1), 36-45
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 55
REFERENCE(S): (1) Abratt, V; Mol Gen Genet 1998, V258, P363 HCAPLUS
(2) Aoki, H; J Biol Chem 1997, V272, P32254 HCAPLUS
(3) Aoki, H; Nucleic Acids Res 1991, V19, P6215 HCAPLUS
(6) Banta, L; J Bacteriol 1998, V180, P6597 HCAPLUS
(7) Becker, A; Gene 1995, V162, P37 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2001 ACS
TI Re-annotating the Mycoplasma pneumoniae genome sequence: adding value, function and reading frames
AB Four years after the original sequence submission, we have re-annotated the genome of Mycoplasma pneumoniae to incorporate novel data. The total no. of ORFss has been increased from 677 to 688 (10 new proteins were predicted in intergenic regions, two further were newly identified by mass spectrometry and one protein ORF was dismissed) and the no. of RNAs from 39 to 42 genes. For 19 of the now 35 tRNAs and for six other functional RNAs the exact genome positions were re-annotated and two new tRNALeu and a small 200 nt RNA were identified. Sixteen protein reading frames were extended and eight shortened. For each ORF a consistent annotation vocabulary has been introduced. Annotation reasoning, annotation categories and comparisons to other published data on M. pneumoniae functional assignments are given. Exptl. evidence includes 2-dimensional gel electrophoresis in combination with mass spectrometry as well as gene expression data from this study. Compared to the original annotation, we increased the no. of proteins with predicted functional features from 349 to 458. The increase includes 36 new predictions and 73 protein assignments confirmed by the published literature. Furthermore, there are 23 redns. and 30 addns. with respect to the previous annotation. MRNA expression data support transcription of 184 of the functionally unassigned reading frames.
ACCESSION NUMBER: 2000:679263 HCAPLUS
DOCUMENT NUMBER: 134:188814
TITLE: Re-annotating the Mycoplasma pneumoniae genome sequence: adding value, function and reading frames
AUTHOR(S): Dandekar, Thomas; Huynen, Martijn; Regula, Jorg Thomas; Ueberle, Barbara; Zimmermann, Carl Ulrich; Andrade, Miguel A.; Doerks, Tobias; Sanchez-Pulido, Luis; Snel, Berend; Suyama, Mikita; Yuan, Yan P.; Herrmann, Richard; Bork, Peer
CORPORATE SOURCE: EMBL, Heidelberg, D-69012, Germany
SOURCE: Nucleic Acids Res. (2000), 28(17), 3278-3288
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 44
REFERENCE(S): (1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS

(2) Aravind, L; Trends Biochem Sci 1998, V23, P17 HCAPLUS
(3) Bellgard, M; Gene 1999, V2[redacted] P33 HCAPLUS
(4) Bork, P; J Mol Biol 1998, V283, P707 HCAPLUS
(5) Bork, P; Methods Enzymol 1996, V266, P162 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2001 ACS
TI Assays for modulators of **elongation factor p** activity
AB Disclosed are novel methods of using **elongation factor p** (**efp**) and related constituents of ribosomal complexes which comprise **efp**, the 50S ribosomal subunit, the 30S ribosomal subunit, the 70S initiation complex, and related proteins, cofactors and enzymes. Methods of identifying compds. which modulate prokaryotic **elongation factor p** and modify cell function are described. Both in vitro and in vivo methods for identifying compds. which modulate such constituents and affect cell function are described. Such identified compds., including various antibiotics, which specifically affect cell growth, methods of treating various disorders with such compds., and antiseptics contg. such compds. are described. The present invention is also directed to methods and compds. that modulate prokaryotic **elongation factor p**.

ACCESSION NUMBER: 2000:535370 HCAPLUS
DOCUMENT NUMBER: 133:144893
TITLE: Assays for modulators of **elongation factor p** activity
INVENTOR(S): Poorman, Roger A.; Wells, Peter Andrew; Marotti, Keith R.; Shinabarger, Dean L.
PATENT ASSIGNEE(S): Pharmacia and Upjohn, USA
SOURCE: PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000045177	A1	20000803	WO 1999-US12073	19990528
W: AE, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9942246	A1	20000818	AU 1999-42246	19990528

PRIORITY APPLN. INFO.: US 1999-117473 P 19990127
WO 1999-US12073 W 19990528

REFERENCE COUNT: 4
REFERENCE(S):
(1) Anon; 1998, 13, HCAPLUS
(2) Anon; 1999, 10, HCAPLUS
(3) Aoki, H; JOURNAL OF BIOLOGICAL CHEMISTRY 1997, V272(51), P32254 HCAPLUS
(4) Swaney, S; ANTIMICROBIAL AGENTS AND CHEMOTHERAPY 1998, V42(12), P3251 HCAPLUS

L4 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2001 ACS
TI The gene encoding the **elongation factor P**

protein is essential for viability and is required for protein synthesis

AB **Elongation factor** ([redacted]**EFP**) is a protein that stimulates the peptidyltransferase act[redacted]ty of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N-formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a homologous protein, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (KanR) gene was inserted near the N-terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temp.-sensitive origin of replication. After transformation into a recA+ E. coli strain, temp.-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants contg. the **efp**-KanR gene in the chromosome grew at 33.degree. only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44 .degree.. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44 .degree.. At 44 .degree., mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for protein synthesis.

ACCESSION NUMBER: 1998:26675 HCAPLUS
DOCUMENT NUMBER: 128:151566
TITLE: The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis
AUTHOR(S): Aoki, Hiroyuki; Dekany, Katalin; Adams, Sally-Lin; Ganoza, M. Clelia
CORPORATE SOURCE: Banting and Best Department of Medical Res., Nucleic Acids, Protein Synthesis and Molecular Genetics, Univ. Toronto, Toronto, ON, M5G 1L6, Can.
SOURCE: J. Biol. Chem. (1997), 272(51), 32254-32259
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2001 ACS

TI Cloning, sequencing and overexpression of the gene for prokaryotic factor EF-P involved in peptide bond synthesis

AB A sol. protein EF-P (**elongation factor P**) from Escherichia coli has been purified and shown to stimulate efficient translation and peptide-bond synthesis on native or reconstituted 70 S ribosomes in vitro. Based on the partial amino acid sequence of EF-P, 18- and 24-nucleotide DNA probes were synthesized and used to screen .lambda. phage clones from the Kohara Gene Bank. The entire EF-P gene was detected on .lambda. clone #650, which contains sequences from the 94 min region of the E. coli genome. Two DNA fragments, 3.0 and 0.78 kilobases in length encompassing the gene, were isolated and cloned into pUC18 and pUC19. Partially purified exts. from cells transformed with these plasmids overrepresented a protein which comigrates with EF-P upon SDS-PAGE, and also exhibited increased EF-P mediated peptide-bond synthetic activity. Based on DNA sequence anal. of this gene, the EF-P protein consists of 187 amino acids with a calcd. mol. wt. of 20,447. The sequence and chromosomal location of EF-P establishes it as a unique gene product.

ACCESSION NUMBER: 1993:2559 HCAPLUS
DOCUMENT NUMBER: 118:2559

TITLE: Cloning, sequencing and overexpression of the gene for prokaryotic factor EF-P involved in peptide bond synthesis
AUTHOR(S): Aoki, Hiroyuki; Adams, Sally Lin; Chung, Dae Gyun; Yaguchi, Makoto; Chuang, Shuang En; Ganoza, M. Clelia
CORPORATE SOURCE: Banting and Best Dep. Med. Res., Univ. Toronto, Toronto, ON, Can.
SOURCE: Nucleic Acids Res. (1991), 19(22), 6215-20
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 15 OF 16 BIOSIS COPYRIGHT 2001 BIOSIS
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to **elongation factor P**, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that **elongation factor P** is important but not essential for the growth of Agrobacterium.
ACCESSION NUMBER: 2001:61207 BIOSIS
DOCUMENT NUMBER: PREV200100061207
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR(S): Peng, Wen-Tao; Banta, Lois M.; Charles, Trevor C.; Nester, Eugene W. (1)
CORPORATE SOURCE: (1) Department of Microbiology, University of Washington, Seattle, WA, 98195-7242: gnester@u.washington.edu USA
SOURCE: Journal of Bacteriology, (January, 2001) Vol. 183, No. 1, pp. 36-45. print.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 16 OF 16 BIOSIS COPYRIGHT 2001 BIOSIS
TI The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis.
AB **Elongation factor P** (**EFP**) is a protein that stimulates the peptidyltransferase activity of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N-formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a

homologous protein, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (KanR) gene was inserted near the N-terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temperature-sensitive origin of replication. After transformation into a recA+ E. coli strain, temperature-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants containing the **efp** -KanR gene in the chromosome grew at 33degree C only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44degree C. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44degree C. At 44degree C, mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for protein synthesis.

ACCESSION NUMBER: 1998:83503 BIOSIS
DOCUMENT NUMBER: PREV199800083503
TITLE: The gene encoding the **elongation factor P** protein is essential for viability and is required for protein synthesis.
AUTHOR(S): Aoki, Hiroyuki; Dekany, Katalin; Adams, Sally-Lin; Ganoza, M. Clelia (1)
CORPORATE SOURCE: (1) C.H. Best Inst., Univ. Toronto, Toronto, ON M5G 1L6 Canada
SOURCE: Journal of Biological Chemistry, (Dec. 19, 1997) Vol. 272, No. 51, pp. 32254-32259.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English

=> d his

(FILE 'HOME' ENTERED AT 13:14:58 ON 21 JUN 2001)

FILE 'MEDLINE, USPATFULL, WPIDS, FROSTI, EMBASE, DGENE, JAPIO, FSTA, HCAPLUS, BIOSIS' ENTERED AT 13:15:31 ON 21 JUN 2001

L1 8295 S OXAZOLIDINONE
L2 104 S ELONGATION FACTOR P
L3 755 S EFP
L4 16 S L2 AND L3

=> s l3 and l1

L5 2 L3 AND L1

=> d l5 ti abs ibib t

'T' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid in at least one of the files. Refer to file specific help messages or the STNGUIDE file for information on formats available in individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):end

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L5 ANSWER 1 OF 2 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Identifying a compound which modulates the activity of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.

AN 2000-524303 [47] WPIDS
AB WO 200045177 A UP[redacted] 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the activity of **efp** comprises contacting **efp** with a compound and determining whether the compound modifies activity of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the binding of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled **oxazolidinone** compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled **oxazolidinone** compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an **oxazolidinone** compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN
COUNTRY COUNT: 86
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW

AU 9942246	A	20000818	(200057)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000045177	A1	WO 1999-US12073	19990528
AU 9942246	A	AU 1999-42246	19990528

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 200045177

PRIORITY APPLN. INFO: US 1999-117473 19990127

L5 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2001 ACS
TI Assays for modulators of elongation factor p activity
AB Disclosed are novel methods of using elongation factor p (**efp**) and related constituents of ribosomal complexes which comprise **efp**, the 50S ribosomal subunit, the 30S ribosomal subunit, the 70S initiation complex, and related proteins, cofactors and enzymes. Methods of identifying compds. which modulate prokaryotic elongation factor p and modify cell function are described. Both in vitro and in vivo methods for identifying compds. which modulate such constituents and affect cell function are described. Such identified compds., including various antibiotics, which specifically affect cell growth, methods of treating various disorders with such compds., and antiseptics contg. such compds. are described. The present invention is also directed to methods and compds. that modulate prokaryotic elongation factor p.
ACCESSION NUMBER: 2000:535370 HCAPLUS
DOCUMENT NUMBER: 133:144893

TITLE: Assays for modulators of elongation factor p activity
INVENTOR(S): [redacted]oorman, Roger A.; Wells, Peter Andrew; Marotti, Keith R.; Shinabarger, Dean L.
PATENT ASSIGNEE(S): Pharmacia and Upjohn, USA
SOURCE: PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000045177	A1	20000803	WO 1999-US12073	19990528
W: AE, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9942246	A1	20000818	AU 1999-42246	19990528

PRIORITY APPLN. INFO.: US 1999-117473 P 19990127
WO 1999-US12073 W 19990528

REFERENCE COUNT: 4
REFERENCE(S):
(1) Anon; 1998, 13, HCAPLUS
(2) Anon; 1999, 10, HCAPLUS
(3) Aoki, H; JOURNAL OF BIOLOGICAL CHEMISTRY 1997, V272(51), P32254 HCAPLUS
(4) Swaney, S; ANTIMICROBIAL AGENTS AND CHEMOTHERAPY 1998, V42(12), P3251 HCAPLUS